

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 72.2917 Seconds
(without alignments)
30.389 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	5	2	AAW45954	Aaw45954 Amyloid b
2	5	100.0	5	8	ADO00814	Ado00814 Human amy
3	5	100.0	5	8	ADO43840	Ado43840 Immunogen
4	5	100.0	5	8	ADQ37309	Adq37309 Antifibri
5	5	100.0	6	2	AAW45948	Aaw45948 Amyloid b
6	5	100.0	6	7	ADB75168	Adb75168 Human amy
7	5	100.0	6	8	ADJ71470	Adj71470 N-termina
8	5	100.0	7	2	AAW45943	Aaw45943 Amyloid b

9	5	100.0	7	6	AAE35433	Aae35433	Abeta pep
10	5	100.0	7	6	ADA90149	Ada90149	Anti-Abet
11	5	100.0	7	6	ADA90932	Ada90932	Solid-pha
12	5	100.0	7	6	ADA90148	Ada90148	Anti-Abet
13	5	100.0	7	6	ADA90931	Ada90931	Solid-pha
14	5	100.0	7	8	ADJ71471	Adj71471	N-termina
15	5	100.0	7	8	ADJ71458	Adj71458	N-termina
16	5	100.0	7	8	ADO00815	Ado00815	Human amy
17	5	100.0	7	8	ADO43841	Ado43841	Immunogen
18	5	100.0	7	8	ADQ37257	Adq37257	Vaccine a
19	5	100.0	7	9	ADZ08902	Adz08902	Human bet
20	5	100.0	8	2	AAW45939	Aaw45939	Amyloid b
21	5	100.0	8	8	ADJ71459	Adj71459	N-termina
22	5	100.0	8	8	ADJ71472	Adj71472	N-termina
23	5	100.0	8	8	ADJ71446	Adj71446	N-termina
24	5	100.0	9	8	ADI35864	Adi35864	Amyloid b
25	5	100.0	9	8	ADI35872	Adi35872	Amyloid b
26	5	100.0	9	8	ADI35901	Adi35901	Amyloid b
27	5	100.0	9	8	ADI35916	Adi35916	Amyloid b
28	5	100.0	9	8	ADI35952	Adi35952	Amyloid b
29	5	100.0	9	8	ADI35954	Adi35954	Amyloid b
30	5	100.0	9	8	ADI35974	Adi35974	Amyloid b
31	5	100.0	9	8	ADI35896	Adi35896	Amyloid b
32	5	100.0	9	8	ADI35930	Adi35930	Amyloid b
33	5	100.0	9	8	ADI35996	Adi35996	Amyloid b
34	5	100.0	9	8	ADI36002	Adi36002	Amyloid b
35	5	100.0	9	8	ADI35902	Adi35902	Amyloid b
36	5	100.0	9	8	ADI35905	Adi35905	Amyloid b
37	5	100.0	9	8	ADI35915	Adi35915	Amyloid b
38	5	100.0	9	8	ADI35969	Adi35969	Amyloid b
39	5	100.0	9	8	ADI35984	Adi35984	Amyloid b
40	5	100.0	9	8	ADI35851	Adi35851	Amyloid b
41	5	100.0	9	8	ADI35993	Adi35993	Amyloid b
42	5	100.0	9	8	ADI36007	Adi36007	Amyloid b
43	5	100.0	9	8	ADI35897	Adi35897	Amyloid b
44	5	100.0	9	8	ADI35933	Adi35933	Amyloid b
45	5	100.0	9	8	ADI35934	Adi35934	Amyloid b

ALIGNMENTS

RESULT 1

AAW45954

ID AAW45954 standard; peptide; 5 AA.

XX

AC AAW45954;

XX

DT 25-MAR-2003 (revised)

DT 30-JUN-1998 (first entry)

XX

DE Amyloid beta peptide fragment.

XX

KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW positron emission tomography; PET; Down's syndrome; amyloidosis.

XX

OS Homo sapiens.

Search completed: January 6, 2006, 16:51:40
Job time : 73.2917 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 20.625 Seconds
(without alignments)
20.043 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	5	2	US-09-095-106A-23	Sequence 23, Appl
2	5	100.0	6	2	US-09-095-106A-18	Sequence 18, Appl
3	5	100.0	7	2	US-09-095-106A-14	Sequence 14, Appl
4	5	100.0	8	2	US-09-095-106A-10	Sequence 10, Appl
5	5	100.0	9	2	US-09-095-106A-7	Sequence 7, Appli
6	5	100.0	10	2	US-09-095-106A-2	Sequence 2, Appli
7	5	100.0	10	2	US-09-724-961-14	Sequence 14, Appl
8	5	100.0	10	2	US-09-724-961-15	Sequence 15, Appl

9	5	100.0	10	2	US-09-724-961-16	Sequence 16, Appl
10	5	100.0	10	2	US-09-724-961-17	Sequence 17, Appl
11	5	100.0	10	2	US-09-724-961-18	Sequence 18, Appl
12	5	100.0	10	2	US-09-724-961-19	Sequence 19, Appl
13	5	100.0	10	2	US-09-580-018-14	Sequence 14, Appl
14	5	100.0	10	2	US-09-580-018-15	Sequence 15, Appl
15	5	100.0	10	2	US-09-580-018-16	Sequence 16, Appl
16	5	100.0	10	2	US-09-580-018-17	Sequence 17, Appl
17	5	100.0	10	2	US-09-580-018-18	Sequence 18, Appl
18	5	100.0	10	2	US-09-580-018-19	Sequence 19, Appl
19	5	100.0	10	2	US-09-724-551-14	Sequence 14, Appl
20	5	100.0	10	2	US-09-724-551-15	Sequence 15, Appl
21	5	100.0	10	2	US-09-724-551-16	Sequence 16, Appl
22	5	100.0	10	2	US-09-724-551-17	Sequence 17, Appl
23	5	100.0	10	2	US-09-724-551-18	Sequence 18, Appl
24	5	100.0	10	2	US-09-724-551-19	Sequence 19, Appl
25	5	100.0	10	2	US-09-724-940-14	Sequence 14, Appl
26	5	100.0	10	2	US-09-724-940-15	Sequence 15, Appl
27	5	100.0	10	2	US-09-724-940-16	Sequence 16, Appl
28	5	100.0	10	2	US-09-724-940-17	Sequence 17, Appl
29	5	100.0	10	2	US-09-724-940-18	Sequence 18, Appl
30	5	100.0	10	2	US-09-724-940-19	Sequence 19, Appl
31	5	100.0	11	2	US-08-766-596A-68	Sequence 68, Appl
32	5	100.0	11	2	US-09-623-548A-957	Sequence 957, App
33	5	100.0	11	2	US-09-623-548A-963	Sequence 963, App
34	5	100.0	11	2	US-09-623-548A-990	Sequence 990, App
35	5	100.0	11	2	US-09-657-276-957	Sequence 957, App
36	5	100.0	11	2	US-09-657-276-963	Sequence 963, App
37	5	100.0	11	2	US-09-657-276-990	Sequence 990, App
38	5	100.0	15	1	US-08-609-090-1	Sequence 1, Appli
39	5	100.0	15	1	US-08-612-785B-4	Sequence 4, Appli
40	5	100.0	15	1	US-08-612-785B-37	Sequence 37, Appl
41	5	100.0	15	2	US-08-617-267C-4	Sequence 4, Appli
42	5	100.0	16	1	US-08-302-808-10	Sequence 10, Appl
43	5	100.0	16	1	US-08-659-984A-20	Sequence 20, Appl
44	5	100.0	16	1	US-08-986-948-10	Sequence 10, Appl
45	5	100.0	16	2	US-08-660-531-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
 US-09-095-106A-23
 ; Sequence 23, Application US/09095106A
 ; Patent No. 6331440
 ; GENERAL INFORMATION:
 ; APPLICANT: NORDSTEDT, Christer
 ; APPLICANT: NASLUND, Jan
 ; APPLICANT: THYBERG, Johan
 ; APPLICANT: TJERNBERG, Lars O.
 ; APPLICANT: TERENIUS, Lars
 ; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
 ; FILE REFERENCE: 000500-124
 ; CURRENT APPLICATION NUMBER: US/09/095,106A
 ; CURRENT FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: US 60/009,386

Qy	1	EVHHQ	5
Db	4	EVHHQ	8

Search completed: January 6, 2006, 17:01:10
Job time : 20.625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 45.625 Seconds
(without alignments)
45.790 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	5	3	US-09-850-061A-23	Sequence 23, Appl
2	5	100.0	5	4	US-10-721-774-23	Sequence 23, Appl
3	5	100.0	6	3	US-09-850-061A-18	Sequence 18, Appl
4	5	100.0	6	4	US-10-084-380A-9	Sequence 9, Appli
5	5	100.0	6	4	US-10-721-774-18	Sequence 18, Appl
6	5	100.0	6	5	US-10-625-854-133	Sequence 133, App
7	5	100.0	7	3	US-09-867-847-6	Sequence 6, Appli
8	5	100.0	7	3	US-09-850-061A-14	Sequence 14, Appl

Search completed: January 6, 2006, 17:05:00
Job time : 46.625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 3.125 Seconds
(without alignments)
13.579 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	28	6	US-10-250-581-2	Sequence 2, Appli
2	5	100.0	28	6	US-10-250-581-5	Sequence 5, Appli
3	5	100.0	28	6	US-10-250-581-8	Sequence 8, Appli
4	5	100.0	28	6	US-10-250-581-11	Sequence 11, Appl
5	5	100.0	28	6	US-10-250-581-14	Sequence 14, Appl

6	5	100.0	28	6	US-10-250-581-17	Sequence 17, Appl
7	5	100.0	28	6	US-10-250-581-2	Sequence 2, Appli
8	5	100.0	28	6	US-10-250-581-5	Sequence 5, Appli
9	5	100.0	28	6	US-10-250-581-8	Sequence 8, Appli
10	5	100.0	28	6	US-10-250-581-11	Sequence 11, Appl
11	5	100.0	28	6	US-10-250-581-14	Sequence 14, Appl
12	5	100.0	28	6	US-10-250-581-17	Sequence 17, Appl
13	5	100.0	40	6	US-10-250-581-3	Sequence 3, Appli
14	5	100.0	40	6	US-10-250-581-6	Sequence 6, Appli
15	5	100.0	40	6	US-10-250-581-9	Sequence 9, Appli
16	5	100.0	40	6	US-10-250-581-12	Sequence 12, Appl
17	5	100.0	40	6	US-10-250-581-15	Sequence 15, Appl
18	5	100.0	40	6	US-10-250-581-18	Sequence 18, Appl
19	5	100.0	40	6	US-10-250-581-3	Sequence 3, Appli
20	5	100.0	40	6	US-10-250-581-6	Sequence 6, Appli
21	5	100.0	40	6	US-10-250-581-9	Sequence 9, Appli
22	5	100.0	40	6	US-10-250-581-12	Sequence 12, Appl
23	5	100.0	40	6	US-10-250-581-15	Sequence 15, Appl
24	5	100.0	40	6	US-10-250-581-18	Sequence 18, Appl
25	5	100.0	40	7	US-11-016-706-36	Sequence 36, Appl
26	5	100.0	40	7	US-11-098-674-12	Sequence 12, Appl
27	5	100.0	42	6	US-10-923-605-1	Sequence 1, Appli
28	5	100.0	42	6	US-10-934-818-1	Sequence 1, Appli
29	5	100.0	42	6	US-10-250-581-4	Sequence 4, Appli
30	5	100.0	42	6	US-10-250-581-7	Sequence 7, Appli
31	5	100.0	42	6	US-10-250-581-10	Sequence 10, Appl
32	5	100.0	42	6	US-10-250-581-13	Sequence 13, Appl
33	5	100.0	42	6	US-10-250-581-16	Sequence 16, Appl
34	5	100.0	42	6	US-10-250-581-19	Sequence 19, Appl
35	5	100.0	42	6	US-10-250-581-4	Sequence 4, Appli
36	5	100.0	42	6	US-10-250-581-7	Sequence 7, Appli
37	5	100.0	42	6	US-10-250-581-10	Sequence 10, Appl
38	5	100.0	42	6	US-10-250-581-13	Sequence 13, Appl
39	5	100.0	42	6	US-10-250-581-16	Sequence 16, Appl
40	5	100.0	42	6	US-10-250-581-19	Sequence 19, Appl
41	5	100.0	42	7	US-11-016-706-37	Sequence 37, Appl
42	5	100.0	43	6	US-10-934-818-6	Sequence 6, Appli
43	5	100.0	43	6	US-10-250-581-1	Sequence 1, Appli
44	5	100.0	43	6	US-10-250-581-1	Sequence 1, Appli
45	5	100.0	438	6	US-10-641-678-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-10-250-581-2

; Sequence 2, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

Search completed: January 6, 2006, 17:05:26
Job time : 3.125 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:43:17 ; Search time 13.9583 Seconds
(without alignments)
34.466 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5	100.0	42	2	PN0512	beta-amyloid prote
2	5	100.0	57	2	A60045	Alzheimer's diseas
3	5	100.0	57	2	F60045	Alzheimer's diseas
4	5	100.0	57	2	D60045	Alzheimer's diseas
5	5	100.0	57	2	E60045	Alzheimer's diseas
6	5	100.0	57	2	G60045	Alzheimer's diseas
7	5	100.0	57	2	B60045	Alzheimer's diseas
8	5	100.0	82	2	PQ0438	Alzheimer's diseas
9	5	100.0	122	2	G98033	hypothetical prote
10	5	100.0	230	2	I39161	dystonin isoform 2

11	5	100.0	284	2	S04723	genome polyprotein
12	5	100.0	306	2	T06642	hypothetical prote
13	5	100.0	313	2	JT0960	polyprotein - pota
14	5	100.0	327	2	S11435	genome polyprotein
15	5	100.0	330	2	A26205	coat protein precu
16	5	100.0	379	2	S13556	genome polyprotein
17	5	100.0	427	2	JA0073	genome polyprotein
18	5	100.0	519	2	PC1072	nuclear inclusion
19	5	100.0	695	1	A49795	Alzheimer's diseas
20	5	100.0	747	2	JH0773	Alzheimer's diseas
21	5	100.0	770	1	QRHUA4	Alzheimer's diseas
22	5	100.0	829	2	C82361	GGDEF family prote
23	5	100.0	846	2	A60678	genome polyprotein
24	5	100.0	1555	2	JT0959	polyprotein - pota
25	5	100.0	3061	1	JN0545	genome polyprotein
26	5	100.0	3063	2	JS0166	genome polyprotein
27	4	80.0	25	2	B34461	heat shock protein
28	4	80.0	57	2	F90778	hypothetical prote
29	4	80.0	73	2	S28480	rfbP protein - Vib
30	4	80.0	78	1	TIZB1A	proteinase inhibit
31	4	80.0	78	1	TIZB1B	proteinase inhibit
32	4	80.0	81	2	E95172	hypothetical prote
33	4	80.0	81	2	E98038	hypothetical prote
34	4	80.0	94	2	B75564	hypothetical prote
35	4	80.0	94	2	F31844	spdA protein - Str
36	4	80.0	101	2	S69296	probable membrane
37	4	80.0	102	2	H75352	hypothetical prote
38	4	80.0	104	2	D95003	hypothetical prote
39	4	80.0	106	2	S59536	cold stress protei
40	4	80.0	106	2	E90196	hypothetical prote
41	4	80.0	115	2	T36957	hypothetical prote
42	4	80.0	117	2	G97875	hypothetical prote
43	4	80.0	117	2	C72691	hypothetical prote
44	4	80.0	122	2	A86900	glutamine syntheta
45	4	80.0	129	2	AF2141	hypothetical prote

ALIGNMENTS

RESULT 1

PN0512

beta-amyloid protein - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: PN0512

R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment for NK-1 substance p receptors.

A;Reference number: PN0512; MUID:93290653; PMID:7685598

A;Accession: PN0512

A;Molecule type: protein

A;Residues: 1-42 <SHI>

A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8

Job time : 20.9583 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 77.0833 Seconds
(without alignments)
45.764 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	33	2	Q9UC33_HUMAN	Q9uc33 homo sapien
2	5	100.0	42	2	Q56JJ6_GRAGR	Q56jj6 grampus gri
3	5	100.0	42	2	Q56JJ7_TURTR	Q56jj7 tursiops tr
4	5	100.0	42	2	Q7M088_CAVPO	Q7m088 cavia porce
5	5	100.0	52	2	Q8WZ99_HUMAN	Q8wz99 homo sapien
6	5	100.0	57	1	A4_URSMA	Q29149 u alzheimer
7	5	100.0	58	1	A4_CANFA	Q28280 c alzheimer
8	5	100.0	58	1	A4_RABIT	Q28748 o alzheimer
9	5	100.0	58	1	A4_SHEEP	Q28757 o alzheimer
10	5	100.0	59	1	A4_BOVIN	Q28053 b alzheimer
11	5	100.0	103	2	Q59YA5_CANAL	Q59ya5 candida alb
12	5	100.0	113	2	Q8JH58_CHESE	Q8jh58 chelydra se
13	5	100.0	122	2	Q8CYL7_STRR6	Q8cyl7 streptococc
14	5	100.0	138	2	Q59Y50_CANAL	Q59y50 candida alb

15	5	100.0	138	2	Q9IZQ7_9POTV	Q9izq7 potato viru
16	5	100.0	153	2	Q4LH81_9BURK	Q4lh81 burkholderi
17	5	100.0	159	2	Q66U39_9DIPT	Q66u39 culicoides
18	5	100.0	159	2	Q66U41_9DIPT	Q66u41 culicoides
19	5	100.0	161	2	Q4HRM6_CAMUP	Q4hrm6 campylobact
20	5	100.0	182	2	Q6EX78_9POTV	Q6ex78 potato viru
21	5	100.0	182	2	Q6EX79_9POTV	Q6ex79 potato viru
22	5	100.0	182	2	Q6EX80_9POTV	Q6ex80 potato viru
23	5	100.0	182	2	Q6EX81_9POTV	Q6ex81 potato viru
24	5	100.0	219	2	Q5MIQ2_AEDAL	Q5miq2 aedes albop
25	5	100.0	256	2	Q5XNP4_AEDAE	Q5xnp4 aedes aegyp
26	5	100.0	259	2	Q7WVV6_STRPN	Q7wvv6 streptococc
27	5	100.0	283	2	Q9EAC3_9POTV	Q9eac3 potato viru
28	5	100.0	284	1	POLG_PVYYO	P11897 potato viru
29	5	100.0	290	2	Q9EAB6_9POTV	Q9eab6 potato viru
30	5	100.0	290	2	Q9EAB7_9POTV	Q9eab7 potato viru
31	5	100.0	290	2	Q9EAB8_9POTV	Q9eab8 potato viru
32	5	100.0	290	2	Q9EAC1_9POTV	Q9eac1 potato viru
33	5	100.0	290	2	Q9EAC6_9POTV	Q9eac6 potato viru
34	5	100.0	290	2	Q9EAD1_9POTV	Q9ead1 potato viru
35	5	100.0	290	2	Q9EAB4_9POTV	Q9eab4 potato viru
36	5	100.0	290	2	Q9EAB5_9POTV	Q9eab5 potato viru
37	5	100.0	290	2	Q9EAB9_9POTV	Q9eab9 potato viru
38	5	100.0	290	2	Q9EAC0_9POTV	Q9eac0 potato viru
39	5	100.0	290	2	Q9EAC4_9POTV	Q9eac4 potato viru
40	5	100.0	290	2	Q9EAC5_9POTV	Q9eac5 potato viru
41	5	100.0	290	2	Q9EAC7_9POTV	Q9eac7 potato viru
42	5	100.0	290	2	Q9EAC8_9POTV	Q9eac8 potato viru
43	5	100.0	290	2	Q9EAC9_9POTV	Q9eac9 potato viru
44	5	100.0	290	2	Q9EAD0_9POTV	Q9ead0 potato viru
45	5	100.0	290	2	Q9EAD2_9POTV	Q9ead2 potato viru

ALIGNMENTS

RESULT 1

Q9UC33_HUMAN

ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.

AC Q9UC33;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Beta-amyloid peptide (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;

RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,

RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;

RT "Isolation and quantification of soluble Alzheimer's beta-peptide from

RT biological fluids.";

RL Nature 359:325-327(1992).

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 101.208 Seconds
(without alignments)
30.389 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	7	100.0	7	8	ADO00815	Ado00815	Human amy
2	7	100.0	7	8	ADO43841	Ado43841	Immunogen
3	6	85.7	6	2	AAW45948	Aaw45948	Amyloid b
4	6	85.7	7	2	AAW45943	Aaw45943	Amyloid b
5	6	85.7	7	6	AAE35433	Aae35433	Abeta pep
6	6	85.7	7	6	ADA90149	Ada90149	Anti-Abet
7	6	85.7	7	6	ADA90932	Ada90932	Solid-pha
8	6	85.7	7	8	ADJ71471	Adj71471	N-termina

9	6	85.7	7	8	ADQ37257	Adq37257 Vaccine a
10	6	85.7	7	9	ADZ08902	Adz08902 Human bet
11	6	85.7	8	2	AAW45939	Aaw45939 Amyloid b
12	6	85.7	8	8	ADJ71459	Adj71459 N-termina
13	6	85.7	8	8	ADJ71472	Adj71472 N-termina
14	6	85.7	9	8	ADI35864	Adi35864 Amyloid b
15	6	85.7	9	8	ADI35872	Adi35872 Amyloid b
16	6	85.7	9	8	ADI35901	Adi35901 Amyloid b
17	6	85.7	9	8	ADI35916	Adi35916 Amyloid b
18	6	85.7	9	8	ADI35952	Adi35952 Amyloid b
19	6	85.7	9	8	ADI35954	Adi35954 Amyloid b
20	6	85.7	9	8	ADI35974	Adi35974 Amyloid b
21	6	85.7	9	8	ADI35896	Adi35896 Amyloid b
22	6	85.7	9	8	ADI35930	Adi35930 Amyloid b
23	6	85.7	9	8	ADI35996	Adi35996 Amyloid b
24	6	85.7	9	8	ADI36002	Adi36002 Amyloid b
25	6	85.7	9	8	ADI35902	Adi35902 Amyloid b
26	6	85.7	9	8	ADI35905	Adi35905 Amyloid b
27	6	85.7	9	8	ADI35915	Adi35915 Amyloid b
28	6	85.7	9	8	ADI35969	Adi35969 Amyloid b
29	6	85.7	9	8	ADI35984	Adi35984 Amyloid b
30	6	85.7	9	8	ADI35851	Adi35851 Amyloid b
31	6	85.7	9	8	ADI35993	Adi35993 Amyloid b
32	6	85.7	9	8	ADI36007	Adi36007 Amyloid b
33	6	85.7	9	8	ADI35897	Adi35897 Amyloid b
34	6	85.7	9	8	ADI35933	Adi35933 Amyloid b
35	6	85.7	9	8	ADI35934	Adi35934 Amyloid b
36	6	85.7	9	8	ADI35863	Adi35863 Amyloid b
37	6	85.7	9	8	ADI35911	Adi35911 Amyloid b
38	6	85.7	9	8	ADI35929	Adi35929 Amyloid b
39	6	85.7	9	8	ADI35948	Adi35948 Amyloid b
40	6	85.7	9	8	ADI35959	Adi35959 Amyloid b
41	6	85.7	9	8	ADI36022	Adi36022 Amyloid b
42	6	85.7	9	8	ADI35892	Adi35892 Amyloid b
43	6	85.7	9	8	ADI36026	Adi36026 Amyloid b
44	6	85.7	9	8	ADI35965	Adi35965 Amyloid b
45	6	85.7	9	8	ADI35881	Adi35881 Amyloid b

ALIGNMENTS

RESULT 1

ADO00815

ID ADO00815 standard; peptide; 7 AA.

XX

AC ADO00815;

XX

DT 01-JUL-2004 (first entry)

XX

DE Human amyloid beta_11 cleavage site, SEQ ID 2.

XX

KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;

KW beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;

KW cleavage site; immunogen; human.

XX

OS Homo sapiens.

Search completed: January 6, 2006, 16:51:40
Job time : 101.208 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 28.875 Seconds
(without alignments)
20.043 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6	85.7	6	2	US-09-095-106A-18	Sequence 18, Appl
2	6	85.7	7	2	US-09-095-106A-14	Sequence 14, Appl
3	6	85.7	8	2	US-09-095-106A-10	Sequence 10, Appl
4	6	85.7	9	2	US-09-095-106A-7	Sequence 7, Appli
5	6	85.7	10	2	US-09-095-106A-2	Sequence 2, Appli
6	6	85.7	10	2	US-09-724-961-15	Sequence 15, Appl
7	6	85.7	10	2	US-09-724-961-16	Sequence 16, Appl
8	6	85.7	10	2	US-09-724-961-17	Sequence 17, Appl

9	6	85.7	10	2	US-09-724-961-18	Sequence 18, Appl
10	6	85.7	10	2	US-09-724-961-19	Sequence 19, Appl
11	6	85.7	10	2	US-09-580-018-15	Sequence 15, Appl
12	6	85.7	10	2	US-09-580-018-16	Sequence 16, Appl
13	6	85.7	10	2	US-09-580-018-17	Sequence 17, Appl
14	6	85.7	10	2	US-09-580-018-18	Sequence 18, Appl
15	6	85.7	10	2	US-09-580-018-19	Sequence 19, Appl
16	6	85.7	10	2	US-09-724-551-15	Sequence 15, Appl
17	6	85.7	10	2	US-09-724-551-16	Sequence 16, Appl
18	6	85.7	10	2	US-09-724-551-17	Sequence 17, Appl
19	6	85.7	10	2	US-09-724-551-18	Sequence 18, Appl
20	6	85.7	10	2	US-09-724-551-19	Sequence 19, Appl
21	6	85.7	10	2	US-09-724-940-15	Sequence 15, Appl
22	6	85.7	10	2	US-09-724-940-16	Sequence 16, Appl
23	6	85.7	10	2	US-09-724-940-17	Sequence 17, Appl
24	6	85.7	10	2	US-09-724-940-18	Sequence 18, Appl
25	6	85.7	10	2	US-09-724-940-19	Sequence 19, Appl
26	6	85.7	11	2	US-08-766-596A-68	Sequence 68, Appl
27	6	85.7	11	2	US-09-623-548A-957	Sequence 957, App
28	6	85.7	11	2	US-09-623-548A-963	Sequence 963, App
29	6	85.7	11	2	US-09-623-548A-990	Sequence 990, App
30	6	85.7	11	2	US-09-657-276-957	Sequence 957, App
31	6	85.7	11	2	US-09-657-276-963	Sequence 963, App
32	6	85.7	11	2	US-09-657-276-990	Sequence 990, App
33	6	85.7	15	1	US-08-612-785B-4	Sequence 4, Appli
34	6	85.7	15	1	US-08-612-785B-37	Sequence 37, Appl
35	6	85.7	15	2	US-08-617-267C-4	Sequence 4, Appli
36	6	85.7	16	1	US-08-302-808-10	Sequence 10, Appl
37	6	85.7	16	1	US-08-659-984A-20	Sequence 20, Appl
38	6	85.7	16	1	US-08-986-948-10	Sequence 10, Appl
39	6	85.7	16	2	US-08-660-531-20	Sequence 20, Appl
40	6	85.7	16	2	US-09-404-578-20	Sequence 20, Appl
41	6	85.7	17	2	US-09-102-451-2	Sequence 2, Appli
42	6	85.7	17	2	US-09-594-366-2	Sequence 2, Appli
43	6	85.7	17	2	US-09-594-366-3	Sequence 3, Appli
44	6	85.7	17	2	US-09-992-800-2	Sequence 2, Appli
45	6	85.7	17	2	US-09-992-800-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
 US-09-095-106A-18
 ; Sequence 18, Application US/09095106A
 ; Patent No. 6331440
 ; GENERAL INFORMATION:
 ; APPLICANT: NORDSTEDT, Christer
 ; APPLICANT: NASLUND, Jan
 ; APPLICANT: THYBERG, Johan
 ; APPLICANT: TJERNBERG, Lars O.
 ; APPLICANT: TERENIUS, Lars
 ; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
 ; FILE REFERENCE: 000500-124
 ; CURRENT APPLICATION NUMBER: US/09/095,106A
 ; CURRENT FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: US 60/009,386

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 63.875 Seconds
(without alignments)
45.790 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
			DB				
1	6	85.7	6	3	US-09-850-061A-18	Sequence 18, Appl	
2	6	85.7	6	4	US-10-721-774-18	Sequence 18, Appl	
3	6	85.7	7	3	US-09-867-847-6	Sequence 6, Appli	
4	6	85.7	7	3	US-09-850-061A-14	Sequence 14, Appl	
5	6	85.7	7	4	US-10-721-774-14	Sequence 14, Appl	
6	6	85.7	7	5	US-10-825-958-6	Sequence 6, Appli	
7	6	85.7	7	5	US-10-810-881A-127	Sequence 127, App	
8	6	85.7	7	5	US-10-505-313-264	Sequence 264, App	
9	6	85.7	7	5	US-10-625-854-134	Sequence 134, App	
10	6	85.7	8	3	US-09-850-061A-10	Sequence 10, Appl	
11	6	85.7	8	4	US-10-721-774-10	Sequence 10, Appl	
12	6	85.7	8	5	US-10-625-854-122	Sequence 122, App	
13	6	85.7	8	5	US-10-625-854-135	Sequence 135, App	
14	6	85.7	9	3	US-09-850-061A-7	Sequence 7, Appli	

15	6	85.7	9	4	US-10-619-454-5	Sequence 5, Appli
16	6	85.7	9	4	US-10-619-454-17	Sequence 17, Appl
17	6	85.7	9	4	US-10-619-454-18	Sequence 18, Appl
18	6	85.7	9	4	US-10-619-454-26	Sequence 26, Appl
19	6	85.7	9	4	US-10-619-454-35	Sequence 35, Appl
20	6	85.7	9	4	US-10-619-454-41	Sequence 41, Appl
21	6	85.7	9	4	US-10-619-454-46	Sequence 46, Appl
22	6	85.7	9	4	US-10-619-454-47	Sequence 47, Appl
23	6	85.7	9	4	US-10-619-454-50	Sequence 50, Appl
24	6	85.7	9	4	US-10-619-454-51	Sequence 51, Appl
25	6	85.7	9	4	US-10-619-454-55	Sequence 55, Appl
26	6	85.7	9	4	US-10-619-454-56	Sequence 56, Appl
27	6	85.7	9	4	US-10-619-454-59	Sequence 59, Appl
28	6	85.7	9	4	US-10-619-454-65	Sequence 65, Appl
29	6	85.7	9	4	US-10-619-454-69	Sequence 69, Appl
30	6	85.7	9	4	US-10-619-454-70	Sequence 70, Appl
31	6	85.7	9	4	US-10-619-454-83	Sequence 83, Appl
32	6	85.7	9	4	US-10-619-454-84	Sequence 84, Appl
33	6	85.7	9	4	US-10-619-454-87	Sequence 87, Appl
34	6	85.7	9	4	US-10-619-454-88	Sequence 88, Appl
35	6	85.7	9	4	US-10-619-454-95	Sequence 95, Appl
36	6	85.7	9	4	US-10-619-454-96	Sequence 96, Appl
37	6	85.7	9	4	US-10-619-454-102	Sequence 102, App
38	6	85.7	9	4	US-10-619-454-106	Sequence 106, App
39	6	85.7	9	4	US-10-619-454-108	Sequence 108, App
40	6	85.7	9	4	US-10-619-454-113	Sequence 113, App
41	6	85.7	9	4	US-10-619-454-119	Sequence 119, App
42	6	85.7	9	4	US-10-619-454-123	Sequence 123, App
43	6	85.7	9	4	US-10-619-454-128	Sequence 128, App
44	6	85.7	9	4	US-10-619-454-138	Sequence 138, App
45	6	85.7	9	4	US-10-619-454-145	Sequence 145, App

ALIGNMENTS

RESULT 1

US-09-850-061A-18

; Sequence 18, Application US/09850061A

; Patent No. US20020094957A1

; GENERAL INFORMATION:

; APPLICANT: NORDSTEDT, Christer

; APPLICANT: NASLUND, Jan

; APPLICANT: THYBERG, Johan

; APPLICANT: TJERNBERG, Lars O.

; APPLICANT: TERENIUS, Lars

; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA

; FILE REFERENCE: 033315-002

; CURRENT APPLICATION NUMBER: US/09/850,061A

; CURRENT FILING DATE: 2001-05-08

; PRIOR APPLICATION NUMBER: US 09/095,106

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: PCT/SE96/01621

; PRIOR FILING DATE: 1996-12-09

; PRIOR APPLICATION NUMBER: SE 9504467-3

; PRIOR FILING DATE: 1995-12-12

; PRIOR APPLICATION NUMBER: US 60/009,386

Search completed: January 6, 2006, 17:05:00
Job time : 63.875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 4.375 Seconds
(without alignments)
13.579 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6	85.7	28	6	US-10-250-581-2	Sequence 2, Appli
2	6	85.7	28	6	US-10-250-581-5	Sequence 5, Appli
3	6	85.7	28	6	US-10-250-581-8	Sequence 8, Appli
4	6	85.7	28	6	US-10-250-581-11	Sequence 11, Appl
5	6	85.7	28	6	US-10-250-581-14	Sequence 14, Appl

6	6	85.7	28	6	US-10-250-581-17	Sequence 17, Appl
7	6	85.7	28	6	US-10-250-581-2	Sequence 2, Appli
8	6	85.7	28	6	US-10-250-581-5	Sequence 5, Appli
9	6	85.7	28	6	US-10-250-581-8	Sequence 8, Appli
10	6	85.7	28	6	US-10-250-581-11	Sequence 11, Appl
11	6	85.7	28	6	US-10-250-581-14	Sequence 14, Appl
12	6	85.7	28	6	US-10-250-581-17	Sequence 17, Appl
13	6	85.7	40	6	US-10-250-581-3	Sequence 3, Appli
14	6	85.7	40	6	US-10-250-581-6	Sequence 6, Appli
15	6	85.7	40	6	US-10-250-581-9	Sequence 9, Appli
16	6	85.7	40	6	US-10-250-581-12	Sequence 12, Appl
17	6	85.7	40	6	US-10-250-581-15	Sequence 15, Appl
18	6	85.7	40	6	US-10-250-581-18	Sequence 18, Appl
19	6	85.7	40	6	US-10-250-581-3	Sequence 3, Appli
20	6	85.7	40	6	US-10-250-581-6	Sequence 6, Appli
21	6	85.7	40	6	US-10-250-581-9	Sequence 9, Appli
22	6	85.7	40	6	US-10-250-581-12	Sequence 12, Appl
23	6	85.7	40	6	US-10-250-581-15	Sequence 15, Appl
24	6	85.7	40	6	US-10-250-581-18	Sequence 18, Appl
25	6	85.7	40	7	US-11-016-706-36	Sequence 36, Appl
26	6	85.7	40	7	US-11-098-674-12	Sequence 12, Appl
27	6	85.7	42	6	US-10-923-605-1	Sequence 1, Appli
28	6	85.7	42	6	US-10-934-818-1	Sequence 1, Appli
29	6	85.7	42	6	US-10-250-581-4	Sequence 4, Appli
30	6	85.7	42	6	US-10-250-581-7	Sequence 7, Appli
31	6	85.7	42	6	US-10-250-581-10	Sequence 10, Appl
32	6	85.7	42	6	US-10-250-581-13	Sequence 13, Appl
33	6	85.7	42	6	US-10-250-581-16	Sequence 16, Appl
34	6	85.7	42	6	US-10-250-581-19	Sequence 19, Appl
35	6	85.7	42	6	US-10-250-581-4	Sequence 4, Appli
36	6	85.7	42	6	US-10-250-581-7	Sequence 7, Appli
37	6	85.7	42	6	US-10-250-581-10	Sequence 10, Appl
38	6	85.7	42	6	US-10-250-581-13	Sequence 13, Appl
39	6	85.7	42	6	US-10-250-581-16	Sequence 16, Appl
40	6	85.7	42	6	US-10-250-581-19	Sequence 19, Appl
41	6	85.7	42	7	US-11-016-706-37	Sequence 37, Appl
42	6	85.7	43	6	US-10-934-818-6	Sequence 6, Appli
43	6	85.7	43	6	US-10-250-581-1	Sequence 1, Appli
44	6	85.7	43	6	US-10-250-581-1	Sequence 1, Appli
45	6	85.7	770	6	US-10-982-545-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-10-250-581-2

; Sequence 2, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

Qy	1	EVHHQK	6
Db	11	EVHHQK	16

Search completed: January 6, 2006, 17:05:26
Job time : 4.375 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:43:17 ; Search time 19.5417 Seconds
(without alignments)
34.466 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	6	85.7	42	2	PN0512		beta-amyloid prote
2	6	85.7	57	2	A60045		Alzheimer's diseas
3	6	85.7	57	2	F60045		Alzheimer's diseas
4	6	85.7	57	2	D60045		Alzheimer's diseas
5	6	85.7	57	2	E60045		Alzheimer's diseas
6	6	85.7	57	2	G60045		Alzheimer's diseas
7	6	85.7	57	2	B60045		Alzheimer's diseas
8	6	85.7	82	2	PQ0438		Alzheimer's diseas
9	6	85.7	695	1	A49795		Alzheimer's diseas
10	6	85.7	747	2	JH0773		Alzheimer's diseas

Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHHQK 6
|||||
Db 53 VHHQK 57

Search completed: January 6, 2006, 16:59:27
Job time : 20.5417 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 107.917 Seconds
(without alignments)
45.764 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6	85.7	33	2	Q9UC33_HUMAN	Q9uc33 homo sapien
2	6	85.7	42	2	Q56JJ6_GRAGR	Q56jj6 grampus gri
3	6	85.7	42	2	Q56JJ7_TURTR	Q56jj7 tursiops tr
4	6	85.7	42	2	Q7M088_CAVPO	Q7m088 cavia porce
5	6	85.7	52	2	Q8WZ99_HUMAN	Q8wz99 homo sapien
6	6	85.7	57	1	A4_URSMA	Q29149 u alzheimer
7	6	85.7	58	1	A4_CANFA	Q28280 c alzheimer
8	6	85.7	58	1	A4_RABIT	Q28748 o alzheimer
9	6	85.7	58	1	A4_SHEEP	Q28757 o alzheimer
10	6	85.7	59	1	A4_BOVIN	Q28053 b alzheimer
11	6	85.7	113	2	Q8JH58_CHESE	Q8jh58 chelydra se
12	6	85.7	219	2	Q5MIQ2_AEDAL	Q5miq2 aedes albop

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 72.2917 Seconds
(without alignments)
30.389 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5	100.0	5	8	ADO00816	Ado00816 Murine am
2	5	100.0	5	8	ADO43842	Ado43842 Immunogen
3	5	100.0	7	8	ADO00817	Ado00817 Murine am
4	5	100.0	7	8	ADO43843	Ado43843 Immunogen
5	5	100.0	20	2	AAR86927	Aar86927 Phage dis
6	5	100.0	24	9	AEB09195	Aeb09195 Human bet
7	5	100.0	26	5	AAE25640	Aae25640 Murine PA
8	5	100.0	26	9	AEB63601	Aeb63601 Poly(ADP-

9	5	100.0	32	2	AAW04402	Aaw04402	Mouse amy
10	5	100.0	32	2	AAW04401	Aaw04401	Mouse amy
11	5	100.0	32	2	AAW04400	Aaw04400	Mouse amy
12	5	100.0	40	4	AAB91786	Aab91786	Amyloid b
13	5	100.0	40	4	AAB91819	Aab91819	Amyloid b
14	5	100.0	40	4	AAB91792	Aab91792	Amyloid b
15	5	100.0	42	1	AAP83153	Aap83153	Lambda SM
16	5	100.0	42	2	AAR10025	Aar10025	Beta-amyl
17	5	100.0	42	2	AAR37867	Aar37867	Beta-amyl
18	5	100.0	42	2	AAR65284	Aar65284	Beta amyl
19	5	100.0	42	2	AAR88206	Aar88206	Rat A42 b
20	5	100.0	42	2	AAR99536	Aar99536	Murine be
21	5	100.0	42	4	AAB91785	Aab91785	Amyloid b
22	5	100.0	42	4	AAB91818	Aab91818	Amyloid b
23	5	100.0	42	4	AAB91791	Aab91791	Amyloid b
24	5	100.0	42	4	AAE03425	Aae03425	Mouse amy
25	5	100.0	42	9	AEA51411	Aea51411	Mouse A 1
26	5	100.0	42	9	AEA62822	Aea62822	Immunocon
27	5	100.0	48	6	ABP97920	Abp97920	Amino aci
28	5	100.0	52	6	ABP97925	Abp97925	Amino aci
29	5	100.0	54	5	ABP06767	Abp06767	Human ORF
30	5	100.0	55	4	AAE12903	Aae12903	Human bet
31	5	100.0	86	8	ADK72155	Adk72155	Antimicro
32	5	100.0	132	2	AAR65290	Aar65290	Rat beta
33	5	100.0	147	4	AAU42003	Aau42003	Propionib
34	5	100.0	147	6	ABM38522	Abm38522	Propionib
35	5	100.0	222	7	ABO77932	Abo77932	Pseudomon
36	5	100.0	226	7	ABO78088	Abo78088	Pseudomon
37	5	100.0	252	6	ABM66089	Abm66089	Propionib
38	5	100.0	304	7	ABO65439	Abo65439	Klebsiell
39	5	100.0	311	8	ADX87946	Adx87946	Plant ful
40	5	100.0	333	4	ABG30295	Abg30295	Novel hum
41	5	100.0	340	8	ADX94914	Adx94914	Plant ful
42	5	100.0	347	3	AAB42568	Aab42568	Human ORF
43	5	100.0	347	4	AAB92675	Aab92675	Human pro
44	5	100.0	347	8	ADX73361	Adx73361	Plant ful
45	5	100.0	354	6	ABU38975	Abu38975	Protein e

ALIGNMENTS

RESULT 1

ADO00816

ID ADO00816 standard; peptide; 5 AA.

XX

AC ADO00816;

XX

DT 01-JUL-2004 (first entry)

XX

DE Murine amyloid beta_11 cleavage site, SEQ ID 3.

XX

KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
 KW beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;
 KW cleavage site; immunogen; murine.

XX

OS Mus sp.

Search completed: January 6, 2006, 16:51:42
Job time : 74.2917 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 20.625 Seconds
(without alignments)
20.043 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	20	2	US-08-253-783-25	Sequence 25, Appl
2	5	100.0	20	4	PCT-US95-06726-25	Sequence 25, Appl
3	5	100.0	26	2	US-09-302-812-21	Sequence 21, Appl
4	5	100.0	26	2	US-09-511-477-21	Sequence 21, Appl
5	5	100.0	26	2	US-09-511-507-21	Sequence 21, Appl
6	5	100.0	26	2	US-09-973-451-21	Sequence 21, Appl
7	5	100.0	40	2	US-09-623-548A-962	Sequence 962, App
8	5	100.0	40	2	US-09-623-548A-968	Sequence 968, App

9	5	100.0	40	2	US-09-623-548A-995	Sequence 995, App
10	5	100.0	40	2	US-09-657-276-962	Sequence 962, App
11	5	100.0	40	2	US-09-657-276-968	Sequence 968, App
12	5	100.0	40	2	US-09-657-276-995	Sequence 995, App
13	5	100.0	42	1	US-08-271-162-5	Sequence 5, Appli
14	5	100.0	42	1	US-08-268-348A-2	Sequence 2, Appli
15	5	100.0	42	2	US-09-623-548A-961	Sequence 961, App
16	5	100.0	42	2	US-09-623-548A-967	Sequence 967, App
17	5	100.0	42	2	US-09-623-548A-994	Sequence 994, App
18	5	100.0	42	2	US-09-657-276-961	Sequence 961, App
19	5	100.0	42	2	US-09-657-276-967	Sequence 967, App
20	5	100.0	42	2	US-09-657-276-994	Sequence 994, App
21	5	100.0	42	4	PCT-US95-08302-5	Sequence 5, Appli
22	5	100.0	42	6	5220013-12	Patent No. 5220013
23	5	100.0	42	6	5223482-12	Patent No. 5223482
24	5	100.0	43	6	5187153-12	Patent No. 5187153
25	5	100.0	55	2	US-09-823-153-10	Sequence 10, Appl
26	5	100.0	133	1	US-08-268-348A-8	Sequence 8, Appli
27	5	100.0	140	2	US-09-270-767-37585	Sequence 37585, A
28	5	100.0	140	2	US-09-270-767-52802	Sequence 52802, A
29	5	100.0	222	2	US-09-252-991A-26678	Sequence 26678, A
30	5	100.0	226	2	US-09-252-991A-26834	Sequence 26834, A
31	5	100.0	304	2	US-09-489-039A-11956	Sequence 11956, A
32	5	100.0	422	2	US-09-252-991A-31797	Sequence 31797, A
33	5	100.0	427	2	US-09-252-991A-31877	Sequence 31877, A
34	5	100.0	539	2	US-09-252-991A-21463	Sequence 21463, A
35	5	100.0	695	2	US-09-458-481B-4	Sequence 4, Appli
36	5	100.0	695	2	US-09-458-481B-5	Sequence 5, Appli
37	5	100.0	695	2	US-09-458-481B-6	Sequence 6, Appli
38	5	100.0	752	2	US-09-489-039A-10195	Sequence 10195, A
39	5	100.0	968	2	US-09-302-812-6	Sequence 6, Appli
40	5	100.0	968	2	US-09-511-477-6	Sequence 6, Appli
41	5	100.0	968	2	US-09-511-507-6	Sequence 6, Appli
42	5	100.0	968	2	US-09-973-451-6	Sequence 6, Appli
43	4	80.0	10	2	US-09-139-762A-32	Sequence 32, Appl
44	4	80.0	10	2	US-09-139-762A-44	Sequence 44, Appl
45	4	80.0	10	2	US-09-139-762A-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-08-253-783-25

; Sequence 25, Application US/08253783

; Patent No. 6719972

; GENERAL INFORMATION:

; APPLICANT: John G. Gribben, Gordon J. Freeman, Lee M. Nadler, Paul

; TITLE OF INVENTION: Ligands for Induction of Antigen Specific

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, suite 510

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109-1875

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-961

Query Match 100.0%; Score 5; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRHQ 5
| | | |
Db 11 EVRHQ 15

Search completed: January 6, 2006, 17:01:11
Job time : 21.625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 45.625 Seconds
(without alignments)
45.790 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	20	4	US-10-732-847A-24	Sequence 24, Appl
2	5	100.0	20	4	US-10-732-847A-25	Sequence 25, Appl
3	5	100.0	24	5	US-10-728-246-6	Sequence 6, Appli
4	5	100.0	26	3	US-09-973-451-21	Sequence 21, Appl
5	5	100.0	26	6	US-11-058-995-21	Sequence 21, Appl
6	5	100.0	40	6	US-11-066-697-962	Sequence 962, App
7	5	100.0	40	6	US-11-066-697-968	Sequence 968, App
8	5	100.0	40	6	US-11-066-697-995	Sequence 995, App

```
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Human Beta App Fragment
US-09-823-153-10
```

```
Query Match          100.0%; Score 5; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 37;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EVRHQ 5
        |||||
Db      11 EVRHQ 15
```

```
RESULT 15
US-10-713-981-10
; Sequence 10, Application US/10713981
; Publication No. US20040121411A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitsky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN
COMPLEX AND
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004 DIV
; CURRENT APPLICATION NUMBER: US/10/713,981
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Human Beta App Fragment
US-10-713-981-10
```

```
Query Match          100.0%; Score 5; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 37;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EVRHQ 5
        |||||
Db      11 EVRHQ 15
```

Search completed: January 6, 2006, 17:05:00
Job time : 45.625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 3.125 Seconds
(without alignments)
13.579 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4	80.0	67	6	US-10-467-657-8570 Sequence 8570, Ap
2	4	80.0	77	6	US-10-467-657-3648 Sequence 3648, Ap
3	4	80.0	89	6	US-10-467-657-9016 Sequence 9016, Ap
4	4	80.0	91	7	US-11-074-176-352 Sequence 352, App
5	4	80.0	95	7	US-11-074-176-180 Sequence 180, App
6	4	80.0	120	6	US-10-793-626-1518 Sequence 1518, Ap

Query Match 80.0%; Score 4; DB 6; Length 240;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VRHQ 5
|||
Db 15 VRHQ 18

RESULT 14

US-10-793-626-2310
; Sequence 2310, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2310
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (250)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2310

Query Match 80.0%; Score 4; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRH 4
|||
Db 176 EVRH 179

RESULT 15

US-10-118-590-36
; Sequence 36, Application US/10118590
; Publication No. US20050277761A1
; GENERAL INFORMATION:
; APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070
; CURRENT APPLICATION NUMBER: US/10/118,590
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/298,731
; PRIOR FILING DATE: 1999-04-23

; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-118-590-36

Query Match 80.0%; Score 4; DB 6; Length 256;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VRHQ 5
|||
Db 72 VRHQ 75

A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648;
 NID:g55616; PIDN:CAA30488.1; PID:g55617
 R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988
 A;Title: Amyloid beta protein precursor is possibly a heparan sulfate
 proteoglycan core protein.
 A;Reference number: A41245; MUID:88264430; PMID:2968652
 A;Accession: A41245
 A;Molecule type: protein
 A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
 A;Cross-references: UNIPARC:UPI00001777FD
 A;Note: evidence for heparan sulfate attachment
 R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994
 A;Title: The beta-A4 amyloid precursor protein binding to copper.
 A;Reference number: S46251; MUID:94320627; PMID:7913895
 A;Contents: annotation; copper binding sites
 A;Note: rat peptides were isolated but not sequenced
 R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991
 A;Title: Purification and tissue level of the beta-amyloid peptide precursor of
 rat brain.
 A;Reference number: A39820; MUID:91217087; PMID:1673681
 A;Accession: A39820
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 18-32 <POT>
 A;Cross-references: UNIPARC:UPI00001777FE
 A;Experimental source: brain
 C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
 plaques is characteristic of both Alzheimer's disease and Down's syndrome.
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
 proteinase inhibitor homology
 C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 5; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRHQ 5
 |||||
 Db 607 EVRHQ 611

Search completed: January 6, 2006, 16:59:29
Job time : 15.9583 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 77.0833 Seconds
(without alignments)
45.764 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5	100.0	79	2	O35463_CRIGR	O35463 cricetulus
2	5	100.0	131	2	Q9NTB8_HUMAN	Q9ntb8 homo sapien
3	5	100.0	141	2	Q4Q224_LEIMA	Q4q224 leishmania
4	5	100.0	197	2	P95796_SERMA	P95796 serratia ma
5	5	100.0	200	2	Q8GWW9_ARATH	Q8gww9 arabidopsis
6	5	100.0	215	2	Q920F7_MOUSE	Q920f7 mus musculu
7	5	100.0	218	2	Q8BPV5_MOUSE	Q8bpv5 mus musculu
8	5	100.0	221	2	Q9M7C8_TARER	Q9m7c8 tagetes ere
9	5	100.0	233	1	MTGA_SHEON	Q8eb02 shewanella
10	5	100.0	237	1	PSD_NOCFA	Q5ynv8 nocardia fa
11	5	100.0	258	2	Q9EQ67_MOUSE	Q9eq67 mus musculu
12	5	100.0	259	2	Q920F8_MOUSE	Q920f8 mus musculu

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 101.208 Seconds
 (without alignments)
 30.389 Million cell updates/sec

Title: US-10-528-928-4
 Perfect score: 7
 Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	7	8	ADO00817	Ado00817 Murine am
2	7	100.0	7	8	ADO43843	Ado43843 Immunogen
3	7	100.0	24	9	AEB09195	Aeb09195 Human bet
4	7	100.0	40	4	AAB91786	Aab91786 Amyloid b
5	7	100.0	40	4	AAB91819	Aab91819 Amyloid b
6	7	100.0	40	4	AAB91792	Aab91792 Amyloid b
7	7	100.0	42	1	AAP83153	Aap83153 Lambda SM
8	7	100.0	42	2	AAR10025	Aar10025 Beta-amyl

9	7	100.0	42	2	AAR37867	Aar37867	Beta-amyl
10	7	100.0	42	2	AAR65284	Aar65284	Beta amyl
11	7	100.0	42	2	AAR88206	Aar88206	Rat A42 b
12	7	100.0	42	2	AAR99536	Aar99536	Murine be
13	7	100.0	42	4	AAB91785	Aab91785	Amyloid b
14	7	100.0	42	4	AAB91818	Aab91818	Amyloid b
15	7	100.0	42	4	AAB91791	Aab91791	Amyloid b
16	7	100.0	42	4	AAE03425	Aae03425	Mouse amy
17	7	100.0	42	9	AEA51411	Aea51411	Mouse A 1
18	7	100.0	42	9	AEA62822	Aea62822	Immunocon
19	7	100.0	48	6	ABP97920	Abp97920	Amino aci
20	7	100.0	52	6	ABP97925	Abp97925	Amino aci
21	7	100.0	55	4	AAE12903	Aae12903	Human bet
22	7	100.0	132	2	AAR65290	Aar65290	Rat beta
23	7	100.0	695	4	AAE03420	Aae03420	Human amy
24	7	100.0	695	8	ADP80871	Adp80871	Mouse amy
25	7	100.0	744	8	ABO84410	Abo84410	Mouse can
26	6	85.7	32	2	AAW04402	Aaw04402	Mouse amy
27	6	85.7	32	2	AAW04401	Aaw04401	Mouse amy
28	6	85.7	32	2	AAW04400	Aaw04400	Mouse amy
29	6	85.7	1124	9	AEA20348	Aea20348	Novel hum
30	6	85.7	1243	8	ADR14793	Adr14793	Amino aci
31	6	85.7	1243	8	ADS10797	Ads10797	Human the
32	6	85.7	1257	8	ADS12051	Ads12051	Human the
33	5	71.4	5	8	ADO00816	Ado00816	Murine am
34	5	71.4	5	8	ADO43842	Ado43842	Immunogen
35	5	71.4	20	2	AAR86927	Aar86927	Phage dis
36	5	71.4	23	6	ABO12468	Abol12468	Human zin
37	5	71.4	23	6	ABO12467	Abol12467	Human zin
38	5	71.4	23	6	ABO13108	Abol13108	Mouse zin
39	5	71.4	23	6	ABO12535	Abol12535	Human zin
40	5	71.4	23	6	ABO12478	Abol12478	Human zin
41	5	71.4	23	6	ABO13319	Abol13319	Mouse zin
42	5	71.4	26	5	AAE25640	Aae25640	Murine PA
43	5	71.4	26	9	AEB63601	Aeb63601	Poly(ADP-
44	5	71.4	38	4	ABB41876	Abb41876	Peptide #
45	5	71.4	38	4	AAM35675	Aam35675	Peptide #

ALIGNMENTS

RESULT 1

ADO00817

ID ADO00817 standard; peptide; 7 AA.

XX

AC ADO00817;

XX

DT 01-JUL-2004 (first entry)

XX

DE Murine amyloid beta_11 cleavage site, SEQ ID 4.

XX

KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
KW beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;
KW cleavage site; immunogen; murine.

XX

OS Mus sp.

Search completed: January 6, 2006, 16:51:43
Job time : 102.208 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 28.875 Seconds
(without alignments)
20.043 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	40	2	US-09-623-548A-962	Sequence 962, App
2	7	100.0	40	2	US-09-623-548A-968	Sequence 968, App
3	7	100.0	40	2	US-09-623-548A-995	Sequence 995, App
4	7	100.0	40	2	US-09-657-276-962	Sequence 962, App
5	7	100.0	40	2	US-09-657-276-968	Sequence 968, App
6	7	100.0	40	2	US-09-657-276-995	Sequence 995, App
7	7	100.0	42	1	US-08-271-162-5	Sequence 5, Appli
8	7	100.0	42	1	US-08-268-348A-2	Sequence 2, Appli

9	7	100.0	42	2	US-09-623-548A-961	Sequence 961, App
10	7	100.0	42	2	US-09-623-548A-967	Sequence 967, App
11	7	100.0	42	2	US-09-623-548A-994	Sequence 994, App
12	7	100.0	42	2	US-09-657-276-961	Sequence 961, App
13	7	100.0	42	2	US-09-657-276-967	Sequence 967, App
14	7	100.0	42	2	US-09-657-276-994	Sequence 994, App
15	7	100.0	42	4	PCT-US95-08302-5	Sequence 5, Appli
16	7	100.0	42	6	5220013-12	Patent No. 5220013
17	7	100.0	42	6	5223482-12	Patent No. 5223482
18	7	100.0	43	6	5187153-12	Patent No. 5187153
19	7	100.0	55	2	US-09-823-153-10	Sequence 10, Appl
20	7	100.0	133	1	US-08-268-348A-8	Sequence 8, Appli
21	7	100.0	695	2	US-09-458-481B-4	Sequence 4, Appli
22	7	100.0	695	2	US-09-458-481B-5	Sequence 5, Appli
23	7	100.0	695	2	US-09-458-481B-6	Sequence 6, Appli
24	6	85.7	200	2	US-09-813-742A-6	Sequence 6, Appli
25	5	71.4	20	2	US-08-253-783-25	Sequence 25, Appl
26	5	71.4	20	4	PCT-US95-06726-25	Sequence 25, Appl
27	5	71.4	26	2	US-09-302-812-21	Sequence 21, Appl
28	5	71.4	26	2	US-09-511-477-21	Sequence 21, Appl
29	5	71.4	26	2	US-09-511-507-21	Sequence 21, Appl
30	5	71.4	26	2	US-09-973-451-21	Sequence 21, Appl
31	5	71.4	140	2	US-09-270-767-37585	Sequence 37585, A
32	5	71.4	140	2	US-09-270-767-52802	Sequence 52802, A
33	5	71.4	143	1	US-07-956-700B-43	Sequence 43, Appl
34	5	71.4	143	1	US-08-476-537-43	Sequence 43, Appl
35	5	71.4	143	1	US-08-485-607-43	Sequence 43, Appl
36	5	71.4	143	1	US-08-475-879-43	Sequence 43, Appl
37	5	71.4	143	2	US-09-433-043B-43	Sequence 43, Appl
38	5	71.4	178	2	US-10-104-047-3886	Sequence 3886, Ap
39	5	71.4	222	2	US-09-252-991A-26678	Sequence 26678, A
40	5	71.4	226	2	US-09-252-991A-26834	Sequence 26834, A
41	5	71.4	259	2	US-10-104-047-3455	Sequence 3455, Ap
42	5	71.4	292	2	US-09-198-452A-738	Sequence 738, App
43	5	71.4	299	2	US-09-438-185A-698	Sequence 698, App
44	5	71.4	304	2	US-09-489-039A-11956	Sequence 11956, A
45	5	71.4	319	2	US-09-328-352-7753	Sequence 7753, Ap

ALIGNMENTS

```

RESULT 1
US-09-623-548A-962
; Sequence 962, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110

```


Search completed: January 6, 2006, 17:01:11
Job time : 28.875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 63.875 Seconds
(without alignments)
45.790 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	24	5	US-10-728-246-6	Sequence 6, Appli
2	7	100.0	40	6	US-11-066-697-962	Sequence 962, App
3	7	100.0	40	6	US-11-066-697-968	Sequence 968, App
4	7	100.0	40	6	US-11-066-697-995	Sequence 995, App
5	7	100.0	42	4	US-10-656-624-6	Sequence 6, Appli
6	7	100.0	42	6	US-11-066-697-961	Sequence 961, App
7	7	100.0	42	6	US-11-066-697-967	Sequence 967, App
8	7	100.0	42	6	US-11-066-697-994	Sequence 994, App

9	7	100.0	48	5	US-10-486-265-4	Sequence 4, Appli
10	7	100.0	55	3	US-09-823-153-10	Sequence 10, Appl
11	7	100.0	55	4	US-10-713-981-10	Sequence 10, Appl
12	7	100.0	740	4	US-10-367-094-194	Sequence 194, App
13	5	71.4	20	4	US-10-732-847A-24	Sequence 24, Appl
14	5	71.4	20	4	US-10-732-847A-25	Sequence 25, Appl
15	5	71.4	26	3	US-09-973-451-21	Sequence 21, Appl
16	5	71.4	26	6	US-11-058-995-21	Sequence 21, Appl
17	5	71.4	38	3	US-09-864-761-45198	Sequence 45198, A
18	5	71.4	44	4	US-10-437-963-115742	Sequence 115742,
19	5	71.4	54	4	US-10-425-115-196777	Sequence 196777,
20	5	71.4	69	4	US-10-425-115-306905	Sequence 306905,
21	5	71.4	77	4	US-10-425-115-199646	Sequence 199646,
22	5	71.4	79	3	US-09-764-878-149	Sequence 149, App
23	5	71.4	79	4	US-10-079-854-149	Sequence 149, App
24	5	71.4	85	4	US-10-424-599-191900	Sequence 191900,
25	5	71.4	87	4	US-10-437-963-119403	Sequence 119403,
26	5	71.4	88	4	US-10-424-599-197008	Sequence 197008,
27	5	71.4	92	4	US-10-425-115-317958	Sequence 317958,
28	5	71.4	95	4	US-10-425-115-185189	Sequence 185189,
29	5	71.4	98	4	US-10-425-115-294512	Sequence 294512,
30	5	71.4	102	4	US-10-425-115-192955	Sequence 192955,
31	5	71.4	111	4	US-10-425-115-347947	Sequence 347947,
32	5	71.4	112	4	US-10-425-115-187421	Sequence 187421,
33	5	71.4	113	3	US-09-925-300-1789	Sequence 1789, Ap
34	5	71.4	114	4	US-10-425-115-330643	Sequence 330643,
35	5	71.4	129	4	US-10-424-599-192420	Sequence 192420,
36	5	71.4	136	3	US-09-813-432-29	Sequence 29, Appl
37	5	71.4	136	4	US-10-174-364-29	Sequence 29, Appl
38	5	71.4	136	4	US-10-246-583-29	Sequence 29, Appl
39	5	71.4	136	4	US-10-689-832-29	Sequence 29, Appl
40	5	71.4	140	3	US-09-764-864-1077	Sequence 1077, Ap
41	5	71.4	145	4	US-10-437-963-187560	Sequence 187560,
42	5	71.4	148	4	US-10-424-599-239933	Sequence 239933,
43	5	71.4	152	4	US-10-424-599-185276	Sequence 185276,
44	5	71.4	152	5	US-10-450-763-39809	Sequence 39809, A
45	5	71.4	153	4	US-10-425-114-39975	Sequence 39975, A

ALIGNMENTS

RESULT 1

US-10-728-246-6

; Sequence 6, Application US/10728246

; Publication No. US20050026165A1

; GENERAL INFORMATION:

; APPLICANT: ORSER, Cindy

; APPLICANT: GROSSET, Anne

; APPLICANT: DAVIDSON, Eugene A.

; TITLE OF INVENTION: DETECTION OF CONFORMATIONALLY ALTERED PROTEINS AND PRIONS

; FILE REFERENCE: A28-011

; CURRENT APPLICATION NUMBER: US/10/728,246

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: 10/161,061

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/295,456

Search completed: January 6, 2006, 17:05:01
Job time : 64.875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 4.375 Seconds
(without alignments)
13.579 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4	57.1	19	6	US-10-923-605-5	Sequence 5, Appli
2	4	57.1	19	6	US-10-934-818-5	Sequence 5, Appli
3	4	57.1	40	7	US-11-016-706-36	Sequence 36, Appl
4	4	57.1	40	7	US-11-098-674-12	Sequence 12, Appl
5	4	57.1	42	6	US-10-923-605-1	Sequence 1, Appli
6	4	57.1	42	6	US-10-934-818-1	Sequence 1, Appli

7	4	57.1	42	7	US-11-016-706-37	Sequence 37, Appl
8	4	57.1	43	6	US-10-934-818-6	Sequence 6, Appli
9	4	57.1	43	6	US-10-250-581-1	Sequence 1, Appli
10	4	57.1	43	6	US-10-250-581-1	Sequence 1, Appli
11	4	57.1	65	6	US-10-467-657-9149	Sequence 9149, Ap
12	4	57.1	67	6	US-10-467-657-8570	Sequence 8570, Ap
13	4	57.1	77	6	US-10-467-657-3648	Sequence 3648, Ap
14	4	57.1	89	6	US-10-467-657-9016	Sequence 9016, Ap
15	4	57.1	91	7	US-11-074-176-352	Sequence 352, App
16	4	57.1	95	7	US-11-074-176-180	Sequence 180, App
17	4	57.1	119	6	US-10-467-657-2818	Sequence 2818, Ap
18	4	57.1	120	6	US-10-793-626-1518	Sequence 1518, Ap
19	4	57.1	129	6	US-10-467-657-2600	Sequence 2600, Ap
20	4	57.1	132	6	US-10-980-459-38	Sequence 38, Appl
21	4	57.1	132	6	US-10-980-459-40	Sequence 40, Appl
22	4	57.1	134	6	US-10-793-626-494	Sequence 494, App
23	4	57.1	134	6	US-10-793-626-1364	Sequence 1364, Ap
24	4	57.1	134	6	US-10-980-459-34	Sequence 34, Appl
25	4	57.1	134	7	US-11-091-643-2	Sequence 2, Appli
26	4	57.1	136	6	US-10-842-206-16	Sequence 16, Appl
27	4	57.1	136	6	US-10-842-206-18	Sequence 18, Appl
28	4	57.1	138	6	US-10-793-626-662	Sequence 662, App
29	4	57.1	138	6	US-10-842-206-10	Sequence 10, Appl
30	4	57.1	149	6	US-10-980-459-36	Sequence 36, Appl
31	4	57.1	155	6	US-10-842-206-12	Sequence 12, Appl
32	4	57.1	158	6	US-10-842-206-20	Sequence 20, Appl
33	4	57.1	158	6	US-10-980-459-4	Sequence 4, Appli
34	4	57.1	179	6	US-10-842-206-6	Sequence 6, Appli
35	4	57.1	179	6	US-10-842-206-24	Sequence 24, Appl
36	4	57.1	179	6	US-10-980-459-7	Sequence 7, Appli
37	4	57.1	179	6	US-10-980-459-10	Sequence 10, Appl
38	4	57.1	182	6	US-10-793-626-2836	Sequence 2836, Ap
39	4	57.1	183	6	US-10-793-626-2606	Sequence 2606, Ap
40	4	57.1	183	6	US-10-842-206-14	Sequence 14, Appl
41	4	57.1	185	6	US-10-842-206-8	Sequence 8, Appli
42	4	57.1	188	6	US-10-842-206-40	Sequence 40, Appl
43	4	57.1	188	6	US-10-980-459-32	Sequence 32, Appl
44	4	57.1	189	6	US-10-467-657-3184	Sequence 3184, Ap
45	4	57.1	197	6	US-10-842-206-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
 US-10-923-605-5
 ; Sequence 5, Application US/10923605
 ; Publication No. US20050249727A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Neuralab Limited
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004740US
 ; CURRENT APPLICATION NUMBER: US/10/923,605
 ; CURRENT FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: US/09/322,289
 ; PRIOR FILING DATE: 1999-05-28

Qy 2 VRHQ 5
|||
Db 84 VRHQ 87

RESULT 15

US-11-074-176-352
; Sequence 352, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 352
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-352

Query Match 57.1%; Score 4; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVRH 4
|||
Db 52 EVRH 55

Search completed: January 6, 2006, 17:05:27
Job time : 4.375 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:43:17 ; Search time 19.5417 Seconds
(without alignments)
34.466 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	7	100.0	33	2	S23094	beta-amyloid prote	
2	7	100.0	695	2	A27485	Alzheimer's diseas	
3	7	100.0	695	2	S00550	Alzheimer's diseas	
4	6	85.7	312	2	T23521	hypothetical prote	
5	6	85.7	513	2	T41011	hypothetical prote	
6	6	85.7	964	2	T41547	hypothetical prote	
7	6	85.7	1305	2	T18548	flax rust resistan	
8	5	71.4	85	2	B47354	ygdF protein - Sal	
9	5	71.4	90	2	AB2430	hypothetical prote	
10	5	71.4	131	2	T46455	hypothetical prote	

Db |||||
 143 RHQKL 147

RESULT 15

H72044

ribosomal protein S2 CP0050 [imported] - Chlamydomonas reinhardtii (strains
CWL029 and AR39)

C;Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: H72044; E81619

R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.;
Grimwood, J.; Davis, R.W.; Stephens, R.S.

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: H72044

A;Molecule type: DNA

A;Residues: 1-277 <ARN>

A;Cross-references: UNIPROT:Q9Z7K9; UNIPARC:UPI0000134EF4; GB:AE001652;

GB:AE001363; NID:g4376997; PIDN:AAD18835.1; PID:g4376999

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81619

A;Molecule type: DNA

A;Residues: 1-277 <REA>

A;Cross-references: UNIPARC:UPI0000134EF4; GB:AE002168; GB:AE002161;

NID:g7188982; PIDN:AAF37943.1; PID:g7188989; GSPDB:GN00122; TIGR:CP0050

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: rs2; CP0050

C;Superfamily: Escherichia coli ribosomal protein S2

Query Match 71.4%; Score 5; DB 2; Length 277;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RHQKL 7

|||||

Db 143 RHQKL 147

Search completed: January 6, 2006, 16:59:30
Job time : 20.5417 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 107.917 Seconds
(without alignments)
45.764 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	79	2	O35463_CRIGR	O35463 cricetulus
2	7	100.0	218	2	Q8BPV5_MOUSE	Q8bpv5 mus musculu
3	7	100.0	384	2	Q8BPC7_MOUSE	Q8bpc7 mus musculu
4	7	100.0	695	2	Q6GR78_MOUSE	Q6gr78 mus musculu
5	7	100.0	733	2	Q6P6Q5_RAT	Q6p6q5 rattus norv
6	7	100.0	770	1	A4_MOUSE	P12023 m amyloid b
7	7	100.0	770	1	A4_RAT	P08592 r amyloid b
8	7	100.0	770	2	Q53ZT3_MOUSE	Q53zt3 mus musculu
9	7	100.0	770	2	Q547B7_RAT	Q547b7 rattus norv
10	6	85.7	312	2	Q21373_CAEEL	Q21373 caenorhabdi
11	6	85.7	509	2	Q4V8J1_RAT	Q4v8j1 rattus norv
12	6	85.7	734	2	Q80V47_MOUSE	Q80v47 mus musculu